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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/988,745

DATE: 01/15/2002  
 TIME: 18:58:12

Input Set : N:\Crf3\RULE60\09988745.raw  
 Output Set: N:\CRF3\01152002\I988745.raw

## SEQUENCE LISTING

- 3 (1) GENERAL INFORMATION:  
 5     (i) APPLICANT: LI, Yi and RUBEN, Steven  
 7     (ii) TITLE OF INVENTION: HUMAN AMINE RECEPTOR  
 9     (iii) NUMBER OF SEQUENCES: 10  
 11    (iv) CORRESPONDENCE ADDRESS:  
 12       (A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN AND FOX, P.L.L.C.  
 13       (B) STREET: 1100 NEW YORK AVENUE, NW, SUITE 600  
 14       (C) CITY: WASHINGTON  
 15       (D) STATE: DC  
 16       (E) COUNTRY: UNITED STATES OF AMERICA  
 17       (F) ZIP: 20005-3934
- 19 (v) COMPUTER READABLE FORM:  
 20       (A) MEDIUM TYPE: Floppy disk  
 21       (B) COMPUTER: IBM PC compatible  
 22       (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 23       (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- 25 (vi) CURRENT APPLICATION DATA:  
 26       (A) APPLICATION NUMBER: US/09/988,745  
 27       (B) FILING DATE: 20-Nov-2001  
 28       (C) CLASSIFICATION:
- C--> 29 (vii) PRIOR APPLICATION DATA:  
 30       (A) APPLICATION NUMBER: 09/314,006  
 31       (B) FILING DATE:  
 32  
 34 (viii) ATTORNEY/AGENT INFORMATION:  
 35       (A) NAME: STEFFE, ERIC K  
 36       (B) REGISTRATION NUMBER: 36,688  
 37       (C) REFERENCE/DOCKET NUMBER: 1488.0840001
- 39 (ix) TELECOMMUNICATION INFORMATION:  
 40       (A) TELEPHONE: (202) 371-2600  
 41       (B) TELEFAX: (202) 371-2540
- 44 (2) INFORMATION FOR SEQ ID NO: 1:  
 46    (i) SEQUENCE CHARACTERISTICS:  
 47       (A) LENGTH: 1380 base pairs  
 48       (B) TYPE: nucleic acid  
 49       (C) STRANDEDNESS: double  
 50       (D) TOPOLOGY: linear  
 52    (ii) MOLECULE TYPE: DNA (genomic)  
 55    (ix) FEATURE:  
 56       (A) NAME/KEY: CDS  
 57       (B) LOCATION: 252..1262  
 60    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 62 CTAGAGCTAG CAGGAGTAAC TCTCATGGAA CCTTGGAAAC CATTCTCAA TTGAATTTCA      60  
 64 GGGCACATTT GAATCAGTAC CCAGGGGCAC TGTACTATGC TCCCAGCTGG ACCTTAGTTT      120  
 66 CCTCCTCTC GTTCACCCCT GTGAGTAATT AACAGACAAA ATTTTTTTT TTTTTTTTT      180  
 68 TTTTTTTTT TTTTGCCCT CCAGTGGAGA AGGTGGCCAG TTCTCAGACA GAGGAAGAGT      240  
 70 AGAAAATCATA A ATG AGA GCT GTC TTC ATC CAA GGT GCT GAA GAG CAC CCT      290

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71	Met Arg Ala Val Phe Ile Gln Gly Ala Glu Glu His Pro	
72	1 5 10	
74	GCG GCA TTC TGC TAC CAG GTG AAT GGG TCT TGC CCC AGG ACA GTA CAT	338
75	Ala Ala Phe Cys Tyr Gln Val Asn Gly Ser Cys Pro Arg Thr Val His	
76	15 20 25	
78	ACT CTG GGC ATC CAG TTG GTC ATC TAC CTG ACC TGT GCA GCA GGC ATG	386
79	Thr Leu Gly Ile Gln Leu Val Ile Tyr Leu Thr Cys Ala Ala Gly Met	
80	30 35 40 45	
82	CTG ATT ATC GTG CTA GGG AAT GTA TTT GTG GCA TTT GCT GTG TCC TAC	434
83	Leu Ile Ile Val Leu Gly Asn Val Phe Val Ala Phe Ala Val Ser Tyr	
84	50 55 60	
86	TTC AAA GCG CTT CAC ACG CCC ACC AAC TTC CTG CTG CTC TCC CTG GCC	482
87	Phe Lys Ala Leu His Thr Pro Thr Asn Phe Leu Leu Ser Leu Ala	
88	65 70 75	
90	CTG GCT GAC ATG TTT CTG GGT CTG CTG GTG CTG CCC CTC AGC ACC ATT	530
91	Leu Ala Asp Met Phe Leu Gly Leu Leu Val Leu Pro Leu Ser Thr Ile	
92	80 85 90	
94	CGC TCA GTG GAG AGC TGC TGG TTC TGC GGG GAC TTC CTC TGC CGC CTG	578
95	Arg Ser Val Glu Ser Cys Trp Phe Phe Gly Asp Phe Leu Cys Arg Leu	
96	95 100 105	
98	CAC ACC TAC CTG GAC ACC CTC TTC TGC CTC ACC TCC ATC TTC CAT CTC	626
99	His Thr Tyr Leu Asp Thr Leu Phe Cys Leu Thr Ser Ile Phe His Leu	
100	110 115 120 125	
102	TGT TTC ATT TCC ATT GAC CGC CAC TGT GCC ATC TGT GAC CCC CTG CTC	674
103	Cys Phe Ile Ser Ile Asp Arg His Cys Ala Ile Cys Asp Pro Leu Leu	
104	130 135 140	
106	TAT CCC TCC AAG TTC ACA GTG AGG GTG GCT CTC AGG TAC ATC CTG GCA	722
107	Tyr Pro Ser Lys Phe Thr Val Arg Val Ala Leu Arg Tyr Ile Leu Ala	
108	145 150 155	
110	GGA TGG GGG GTG CCC GCA GCA TAC ACT TCG TTA TTC CTC TAC ACA GAT	770
111	Gly Trp Gly Val Pro Ala Ala Tyr Thr Ser Leu Phe Leu Tyr Thr Asp	
112	160 165 170	
114	GTG GTA GAG ACA AGG CTC AGC CAG TGG CTG GAA GAG ATG CCT TGT GTG	818
115	Val Val Glu Thr Arg Leu Ser Gln Trp Leu Glu Glu Met Pro Cys Val	
116	175 180 185	
118	GGC AGT TGC CAG CTG CTG CTC AAT AAA TTT TGG GGC TGG TTA AAC TTC	866
119	Gly Ser Cys Gln Leu Leu Leu Asn Lys Phe Trp Gly Trp Leu Asn Phe	
120	190 195 200 205	
122	CCT TTG TTC TTT GTC CCC TGC CTC ATT ATG ATC AGC TTG TAT GTG AAG	914
123	Pro Leu Phe Phe Val Pro Cys Leu Ile Met Ile Ser Leu Tyr Val Lys	
124	210 215 220	
126	ATC TTT GTG GTT GCT ACC AGA CAG GCT CAG CAG ATT ACC ACA TTG AGC	962
127	Ile Phe Val Val Ala Thr Arg Gln Ala Gln Gln Ile Thr Thr Leu Ser	
128	225 230 235	
130	AAA AGC CTG GCT GGG GCT GCC AAG CAT GAG AGA AAA GCT GCC AAG ACC	1010
131	Lys Ser Leu Ala Gly Ala Ala Lys His Glu Arg Lys Ala Ala Lys Thr	
132	240 245 250	
134	CTG GGC ATT GTT GTG GGC ATA TAC CTC TTG TGC TGG CTG CCC TTC ACC	1058
135	Leu Gly Ile Val Val Gly Ile Tyr Leu Leu Cys Trp Leu Pro Phe Thr	

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136	255	260	265	
138	ATA GAC ACG ATG GTC GAC AGC CTC CTT CAC TTT ATC ACA CCC CCA CTG			1106
139	Ile Asp Thr Met Val Asp Ser Leu Leu His Phe Ile Thr Pro Pro Leu			
140	270	275	280	285
142	GTC TTT GAC ATC TTT ATC TGG TTT GCT TAC TTC AAC TCA GCC TGC AAC			1154
143	Val Phe Asp Ile Phe Ile Trp Phe Ala Tyr Phe Asn Ser Ala Cys Asn			
144	290	295	300	
146	CCC ATC ATC TAT GTC TTT TCC TAC CAG TGG TTT CGG AAG GCA CTG AAA			1202
147	Pro Ile Ile Tyr Val Phe Ser Tyr Gln Trp Phe Arg Lys Ala Leu Lys			
148	305	310	315	
150	CTC ACA CTG AGC CAG AAG GTC TTC TCA CCG CAG ACA CGC ACT GTT GAT			1250
151	Leu Thr Leu Ser Gln Lys Val Phe Ser Pro Gln Thr Arg Thr Val Asp			
152	320	325	330	
154	TTG TAC CAA GAA TGATTCCCTTC TACTAAATGC AGGCAAGGAG TAGGACCTCA			1302
155	Leu Tyr Gln Glu			
156	335			
158	CAGGAAAGAT AAGTGGCACT GTGACCGCGG GCTGTGTGGT GTTGAGTTG TGGGCATGCT			1362
160	TCCAGGACAG CATGGGTT			1380
163	(2) INFORMATION FOR SEQ ID NO: 2:			
165	(i) SEQUENCE CHARACTERISTICS:			
166	(A) LENGTH: 337 amino acids			
167	(B) TYPE: amino acid			
168	(D) TOPOLOGY: linear			
170	(ii) MOLECULE TYPE: protein			
172	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:			
174	Met Arg Ala Val Phe Ile Gln Gly Ala Glu Glu His Pro Ala Ala Phe			
175	1	5	10	15
177	Cys Tyr Gln Val Asn Gly Ser Cys Pro Arg Thr Val His Thr Leu Gly			
178	20	25	30	
180	Ile Gln Leu Val Ile Tyr Leu Thr Cys Ala Ala Gly Met Leu Ile Ile			
181	35	40	45	
183	Val Leu Gly Asn Val Phe Val Ala Phe Ala Val Ser Tyr Phe Lys Ala			
184	50	55	60	
186	Leu His Thr Pro Thr Asn Phe Leu Leu Ser Leu Ala Leu Ala Asp			
187	65	70	75	80
189	Met Phe Leu Gly Leu Leu Val Leu Pro Leu Ser Thr Ile Arg Ser Val			
190	85	90	95	
192	Glu Ser Cys Trp Phe Phe Gly Asp Phe Leu Cys Arg Leu His Thr Tyr			
193	100	105	110	
195	Leu Asp Thr Leu Phe Cys Leu Thr Ser Ile Phe His Leu Cys Phe Ile			
196	115	120	125	
198	Ser Ile Asp Arg His Cys Ala Ile Cys Asp Pro Leu Leu Tyr Pro Ser			
199	130	135	140	
201	Lys Phe Thr Val Arg Val Ala Leu Arg Tyr Ile Leu Ala Gly Trp Gly			
202	145	150	155	160
204	Val Pro Ala Ala Tyr Thr Ser Leu Phe Leu Tyr Thr Asp Val Val Glu			
205	165	170	175	
207	Thr Arg Leu Ser Gln Trp Leu Glu Glu Met Pro Cys Val Gly Ser Cys			
208	180	185	190	

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210 Gln Leu Leu Leu Asn Lys Phe Trp Gly Trp Leu Asn Phe Pro Leu Phe  
211 195 200 205  
213 Phe Val Pro Cys Leu Ile Met Ile Ser Leu Tyr Val Lys Ile Phe Val  
214 210 215 220  
216 Val Ala Thr Arg Gln Ala Gln Gln Ile Thr Thr Leu Ser Lys Ser Leu  
217 225 230 235 240  
219 Ala Gly Ala Ala Lys His Glu Arg Lys Ala Ala Lys Thr Leu Gly Ile  
220 245 250 255  
222 Val Val Gly Ile Tyr Leu Leu Cys Trp Leu Pro Phe Thr Ile Asp Thr  
223 260 265 270  
225 Met Val Asp Ser Leu Leu His Phe Ile Thr Pro Pro Leu Val Phe Asp  
226 275 280 285  
228 Ile Phe Ile Trp Phe Ala Tyr Phe Asn Ser Ala Cys Asn Pro Ile Ile  
229 290 295 300  
231 Tyr Val Phe Ser Tyr Gln Trp Phe Arg Lys Ala Leu Lys Leu Thr Leu  
232 305 310 315 320  
234 Ser Gln Lys Val Phe Ser Pro Gln Thr Arg Thr Val Asp Leu Tyr Gln  
235 325 330 335  
237 Glu

240 (2) INFORMATION FOR SEQ ID NO: 3:

242 (i) SEQUENCE CHARACTERISTICS:  
243 (A) LENGTH: 29 base pairs  
244 (B) TYPE: nucleic acid  
245 (C) STRANDEDNESS: single  
246 (D) TOPOLOGY: linear

248 (ii) MOLECULE TYPE: DNA (genomic)  
253 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

255 CGGAATTCCCT UATGAGAGCT GTCTTCATC

29

257 (2) INFORMATION FOR SEQ ID NO: 4:

259 (i) SEQUENCE CHARACTERISTICS:  
260 (A) LENGTH: 32 base pairs  
261 (B) TYPE: nucleic acid  
262 (C) STRANDEDNESS: single  
263 (D) TOPOLOGY: linear

265 (ii) MOLECULE TYPE: DNA (genomic)

270 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

272 CGGAAGCTTC GTCATTCTTG GTACAAATCA AC

32

274 (2) INFORMATION FOR SEQ ID NO: 5:

276 (i) SEQUENCE CHARACTERISTICS:  
277 (A) LENGTH: 30 base pairs  
278 (B) TYPE: nucleic acid  
279 (C) STRANDEDNESS: single  
280 (D) TOPOLOGY: linear

282 (ii) MOLECULE TYPE: DNA (genomic)

287 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

289 CGGGATCCCT CCATGAGAGC TGTCTTCATC

30

291 (2) INFORMATION FOR SEQ ID NO: 6:

293 (i) SEQUENCE CHARACTERISTICS:  
294 (A) LENGTH: 29 base pairs

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295 (B) TYPE: nucleic acid  
 296 (C) STRANDEDNESS: single  
 297 (D) TOPOLOGY: linear  
 299 (ii) MOLECULE TYPE: DNA (genomic)  
 304 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
 306 CGGGATCCCG CTCATTCTTG GTACAAATC  
 308 (2) INFORMATION FOR SEQ ID NO: 7:  
 310 (i) SEQUENCE CHARACTERISTICS:  
 311 (A) LENGTH: 34 base pairs  
 312 (B) TYPE: nucleic acid  
 313 (C) STRANDEDNESS: single  
 314 (D) TOPOLOGY: linear  
 316 (ii) MOLECULE TYPE: DNA (genomic)  
 321 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
 323 GTCCAAGCTT GCCACCATGA GAGCTGTCTT CATC  
 325 (2) INFORMATION FOR SEQ ID NO: 8:  
 327 (i) SEQUENCE CHARACTERISTICS:  
 328 (A) LENGTH: 61 base pairs  
 329 (B) TYPE: nucleic acid  
 330 (C) STRANDEDNESS: single  
 331 (D) TOPOLOGY: linear  
 333 (ii) MOLECULE TYPE: DNA (genomic)  
 338 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
 340 CTAGCTCGAG TCAAGCGTAG TCTGGGACGT CGTATGGGTA GCATTCTTGG TACAAATCAA  
 342 C  
 344 (2) INFORMATION FOR SEQ ID NO: 9:  
 346 (i) SEQUENCE CHARACTERISTICS:  
 347 (A) LENGTH: 365 amino acids  
 348 (B) TYPE: amino acid  
 349 (C) STRANDEDNESS: Not Relevant  
 350 (D) TOPOLOGY: Not Relevant  
 352 (ii) MOLECULE TYPE: protein  
 357 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
 359 Ala Arg Leu Leu Val Leu Ala Ser Pro Pro Ala Ser Leu Leu Pro Pro  
 360 1 5 10 15  
 362 Ala Ser Glu Gly Ser Ala Pro Leu Ser Gln Gln Trp Thr Ala Gly Met  
 363 20 25 30  
 365 Gly Leu Leu Val Ala Leu Ile Val Leu Leu Ile Val Val Gly Asn Val  
 366 35 40 45  
 368 Leu Val Ile Val Ala Ile Ala Lys Thr Pro Arg Leu Gln Thr Leu Thr  
 369 50 55 60  
 371 Asn Leu Phe Ile Met Ser Leu Ala Ser Ala Asp Leu Val Met Gly Leu  
 372 65 70 75 80  
 374 Leu Val Val Pro Phe Gly Ala Thr Ile Val Val Trp Gly Arg Trp Glu  
 375 85 90 95  
 377 Tyr Gly Ser Phe Phe Cys Glu Leu Trp Thr Ser Val Asp Val Leu Cys  
 378 100 105 110  
 380 Val Thr Ala Ser Ile Glu Thr Leu Cys Val Ile Ala Leu Asp Arg Tyr  
 381 115 120 125

## VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09988745.raw  
Output Set: N:\CRF3\01152002\I988745.raw

L:26 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:27 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:30 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]  
L:350 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=9